



#### (1) GENERAL INFORMATION:

- (i) APPLICANT:
  - (A) NAME: Rotkreuzstiftung Zentrallaboratorium Blutspendedienst
  - (B) STREET: Wankdorfstrasse 10
  - (C) CITY: Bern 22
  - (E) COUNTRY: Switzerland
  - (F) POSTAL CODE (ZIP): CH-3000
- (ii) TITLE OF INVENTION: Recombinant Fab-fragment with reactivity against Rhesus D antigens, DNA encoding them, complete antibodies comprising the Fab fragments and process for their preparation
- (iii) NUMBER OF SEQUENCES: 64
- (iv) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DØS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
- (v) CURRENT APPLICATION DATA:
  APPLICATION NUMBER: PCT/EP97/03253
- (vi) PRIOR APPLICATION DATA;
  - (A) APPLICATION NUMBER: EP 96810421.6
  - (B) FILING DATE: 24-JUN-1996
- (2) INFORMATION FOR SEQ ID NO: 1:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 375 base pairs
    - (B) TYPE: nycleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA to mRNA
  - (iii) HYPØTHETICAL: NO

(iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: Adult (E) HAPLOTYPE: Diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA Library, LD1 (B) CLONE: LD1-40 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: Chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 295..342) (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..375 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1: CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Arg 15 10 5 1 TCC CTG AGA CTC TCC TGT ATA GCG TCT GGA TTC ACC CTC AGG AAT TAT 96 Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr 30 25 20 GCC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 45 40 35

GCA GGT ATA TGG TTT GAT GGA AGT AAC AAA AAC TAT GCA GAC TCC GTG 192 Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val 50 55 60 AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC ACG CTG TAT 240 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 70 65 75 80 CTG CAA CTG AAC AGC CTG AGA GAC GAG GAC ACG GCT GTG TAT TAT TGT 288 Leu Gln Leu Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys 90 GCG AGA GAG CGA GCA CGT GGT ATT TCT AGG TTC TAT TAC TAC ATG 336 Ala Arg Glu Arg Ala Ala Arg Gly Ile Ser Arg Phe Tyr Tyr Met 100 105 110 GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC CCA 375 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Pro 115 120 125 (2) INFORMATION FOR SEQ ID NO: 2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2: Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Arg 1 5 10 15 Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr 20 25 30 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45 Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val

(C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor

(A) ORGANISM: Homo sapiens

(A) LIBRARY: cDNA library, LD1

(C) UNITS: Chromosome band number

(E) HAPLOTYPE: diploid

(vii) IMMEDIATE SOURCE:

(B) CLONE: LD1-40

(viii) POSITION IN GENOME:

(B) MAP POSITION: p11

(D) DEVELOPMENTAL STAGE: Adult

(G) CELL TYPE: Peripheral lymphocyte B

(A) CHROMOSOME/SEGMENT: Chromosome 2

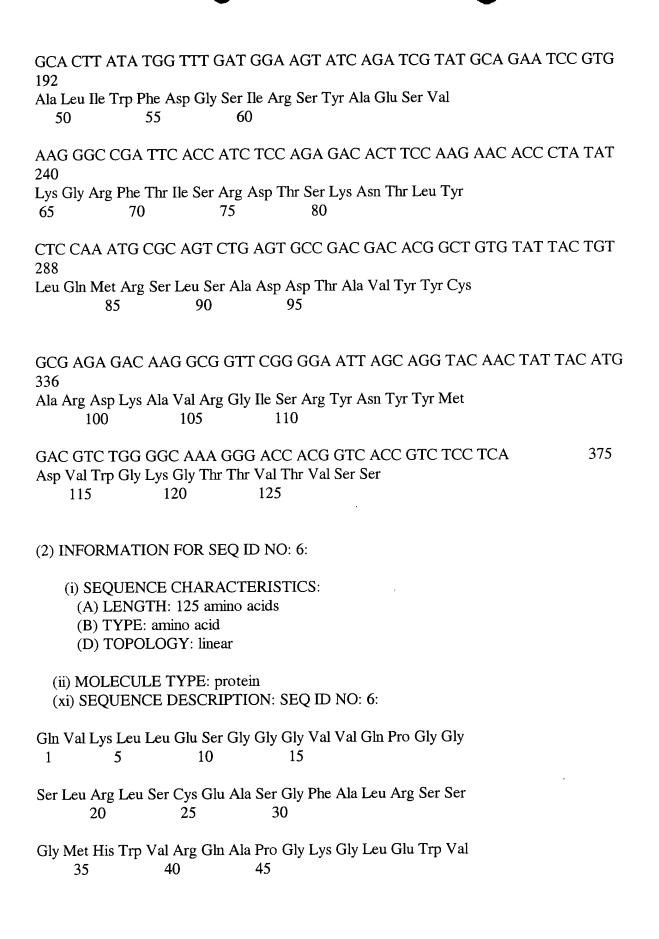
(A) NAME/KEY: CDS (B) LOCATION:1..318 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(64..96, 142..162, 259..288) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3: GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGC GAC AGA Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 10 15 5 1 GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT AGG AGC CAT TTG AAT Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn 30 20 25 TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG TTG CTG ATC TAT GGT 144 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly 40 45 35 GCG TCC ACT TTG CAA AGT GGC GTC CCA TCA AGG TTC AGT GGC AGT GGC Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 60 50 55 TCT GGG GCA GTT TTC ACT CTC ACC ATC GCC AGT CTA CAA CCT GAA GAT Ser Gly Ala Val Phe Thr Leu Thr Ile Ala Ser Leu Gln Pro Glu Asp 80 65 70 75 TTT GCA ACT TAC TGT CAA GAG AGT TAC AGT AAT CCT CTA ATC ACC 288 Phe Ala Thr Tyr Tyr Cys Gln Glu Ser Tyr Ser Asn Pro Leu Ile Thr 95 90 85 318 TTC GGC CAA GGG ACA CGA CTG GAG ACT AAA Phe Gly Gln Gly Thr Arg Leu Glu Thr Lys 100 105

(ix) FEATURE:

(2) INFORMATION FOR SEQ ID NO: 4: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 106 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4: Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 15 5 10 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn 30 20 25 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly 40 45 35 Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 55 60 50 Ser Gly Ala Val Phe Thr Leu Thr Ile Ala Ser Leu Gln Pro Glu Asp 80 70 75 65 Phe Ala Thr Tyr Tyr Cys Gln Glu Ser Tyr Ser Asn Pro Leu Ile Thr 85 90 95 Phe Gly Gln Gly Thr Arg Leu Glu Thr Lys 100 105 (2) INFORMATION FOR SEQ ID NO: 5: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 375 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal
<ul> <li>(vi) ORIGINAL SOURCE:</li> <li>(A) ORGANISM: Homo sapiens</li> <li>(C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor</li> <li>(D) DEVELOPMENTAL STAGE: Adult</li> <li>(E) HAPLOTYPE: diploid</li> <li>(G) CELL TYPE: Peripheral lymphocyte B</li> </ul>
(vii) IMMEDIATE SOURCE:  (A) LIBRARY: cDNA library, LD1  (B) CLONE: LD1-52
<ul> <li>(viii) POSITION IN GENOME:</li> <li>(A) CHROMOSOME/SEGMENT: Chromosome 14</li> <li>(B) MAP POSITION: q32.3</li> <li>(C) UNITS: Chromosome band number</li> </ul>
<ul><li>(ix) FEATURE:</li><li>(A) NAME/KEY: CDS</li><li>(B) LOCATION:1375</li><li>(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"</li></ul>
(ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91105, 148198, 295342)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG 48
Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly  1 5 10 15
TCC CTG AGA CTC TCC TGT GAA GCG TCT GGA TTC GCC CTC AGA AGT TCT 96
Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Ala Leu Arg Ser Ser 20 25 30
GGC ATG CAC TGG GTC CGC CAG GCT CCT GGC AAG GGG CTG GAG TGG GTG 144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45

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Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val 50 55 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr 70 75 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys 90 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 110 105 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 120 125 (2) INFORMATION FOR SEQ ID NO: 7: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 318 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: Adult (E) HAPLOTYPE: Diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA Library, LD1 (B) CLONE: LD1-52 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: Chromosome 2 (B) MAP POSITION: P 11

(C) UNITS: chromosome b.No
<ul><li>(ix) FEATURE:</li><li>(A) NAME/KEY: CDS</li><li>(B) LOCATION:1318</li><li>(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"</li></ul>
(ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(6496, 142162, 259288)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA 48
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 1 5 10 15
GTC ACC ATC ACT TGC CGG GCA AGT CAG AAC ATT ATC CGC TAT TTA AAT 96
Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Ile Arg Tyr Leu Asn 20 25 30
TGG TAT CAG CAG AAG CCA GGG AAA GCC CCT AGG CTC CTG ATC TAT GGT
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Tyr Gly 35 40 45
GCG TCC ACT TTG CAA AGT GGG GTC CCA TCA AGG TTC AGT GGC AGT GGA
Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60
TCT GGG ACA GAT TTC ACT CTC ACC ATC AGT AGT CTG CAA CCT GAA GAT 240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 65 70 75 80
TTT GCA ACT TAC TGT CAA CAG AGT TAC CGT ACC CCT CCA TTC ACT 288
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Pro Phe Thr 85 90 95
TTC GGC CCT GGG ACC AAA GTG GAG ATC AAA 318

Phe Gly Pro Gly Thr Lys Val Glu Ile Lys 100 105

## (2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 106 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Ile Arg Tyr Leu Asn 20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Tyr Gly 35 40 45

Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 65 70 75 80

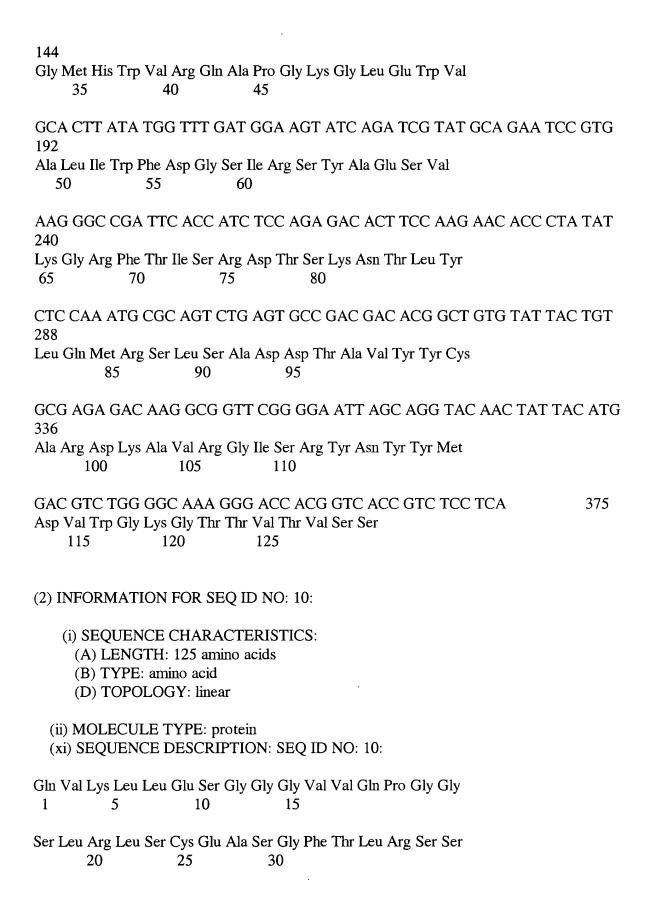
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Pro Phe Thr 85 90 95

Phe Gly Pro Gly Thr Lys Val Glu Ile Lys 100 105

### (2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 375 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: Adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA LIBRARY, LD1 (B) CLONE: LD1-84 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: Chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 295..342) (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..375 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9: CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG 48 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 5 10 15 TCC CTG AGA CTC TCC TGT GAA GCG TCT GGA TTC ACC CTC AGA AGT TCT Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser 25 30 20 GGC ATG CAC TGG GTC CGC CAG GCT CCT GGC AAG GGG CTG GAG TGG GTG



Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45

Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr 65 70 75 80

Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys 85 90 95

Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120 125

#### (2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 315 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
  - (C) INDIVIDUAL ISOLATE: Hyperimmune rhsus D donor
  - (D) DEVELOPMENTAL STAGE: Adult
  - (E) HAPLOTYPE: diploid
  - (G) CELL TYPE: Peripheral lymphocyte B
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA LIBRARY, LD1
  - (B) CLONE: LD1-84

<ul> <li>(viii) POSITION IN GENOME:</li> <li>(A) CHROMOSOME/SEGMENT: Chromosome 2</li> <li>(B) MAP POSITION: p11</li> <li>(C) UNITS: Chromosome band number</li> </ul>
<ul><li>(ix) FEATURE:</li><li>(A) NAME/KEY: CDS</li><li>(B) LOCATION:1315</li><li>(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"</li></ul>
(ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(6496, 142162, 259285)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT ATA GGA GAC AGA
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg  1 5 10 15
GTC ACC ATC ACC TGC CGG GCA AGT CAG AGT ATC ATC AGG TAT TTG AAT 96
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn 20 25 30
TGG TAT CAG CAC AAA CCA GGA AAA GCC CCT AAA CTC CTC ATC TTT GCT
Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Phe Ala 35 40 45
GCA TCG AAT TTG CAA ACT GGG GTC CCA TCC AGG TTC AGT GGC AGT GGA 192
Ala Ser Asn Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60
TCT GGG ACA GAT TTC ACT CTC ACC ATC AGT GAC CTG CAG CCT GAG GAT 240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asp Leu Gln Pro Glu Asp 65 70 75 80
TTC GCA ACT TAC TGT CAA CAG AGT TAC AGT AGG CCG TTC ACT TTT 288
Phe Ala Thr Tyr Cys Gln Gln Ser Tyr Ser Arg Pro Phe Thr Phe

. . . .

GGC CGG GGG ACC AGC CTG GAC ATC AAA
Gly Arg Gly Thr Ser Leu Asp Ile Lys
100 105

315

### (2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid(D) TOPOLOGY: linear

· (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg
1 . 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn 20 25 30

Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Phe Ala 35 40 45

Ala Ser Asn Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asp Leu Gln Pro Glu Asp 65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Arg Pro Phe Thr Phe 85 90 95

Gly Arg Gly Thr Ser Leu Asp Ile Lys 100 105

# (2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

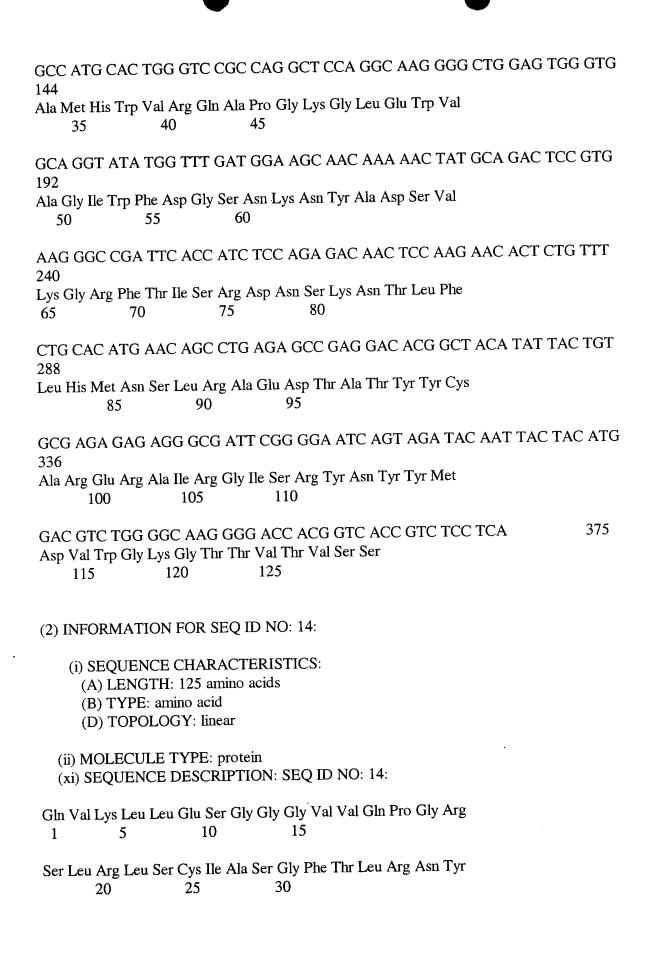
(A) LENGTH: 375 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA LIBRARY, LD1 (B) CLONE: LD1-110 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: Chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..375 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 295..348) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13: CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg 1 5 10 15 TCC CTG AGA CTC TCC TGT ATA GCG TCT GGA TTC ACC CTC AGG AAT TAT 96 Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr 30 25 20



Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 40 35 Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val 55 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe 75 70 Leu His Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Thr Tyr Tyr Cys 90 85 Ala Arg Glu Arg Ala Ile Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 110 105 100 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 120 115 (2) INFORMATION FOR SEQ ID NO: 15: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: Adult (E) HAPLOTYPE: Diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA Library, LD1 (B) CLONE: LD1-110

(viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: Chromosome 2 (B) MAP POSITION: p11 (C) UNITS: chromosome b.No (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..315 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(64..96, 142..162, 259..285) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15: GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 15 10 1 5 GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT CGA AGC TCT TTA AAT 96 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser Ser Leu Asn 30 20 TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAA GTC CTG ATC TAT GCT Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile Tyr Ala 45 35 40 GCA TCC AGT TTG CAA AGT GGG GTC CCA TCC AGG TTC AGT GGC AGA GGA Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly 50 55 TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTG CAG CCT GAA GAT 240 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 80 75 65 TTT GCG ACT TAT TAT TGT CAA CAG AGT TCC AGT TCC TCG TGG ACG TTC Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Ser Ser Ser Trp Thr Phe

85 90 95

GGC CAA GGG ACC AAG GTG GAA ATC AAA Gly Gln Gly Thr Lys Val Glu Ile Lys 100 105 315

# (2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 105 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser Ser Leu Asn 20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile Tyr Ala 35 40 45

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly 50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 65 70 75 80

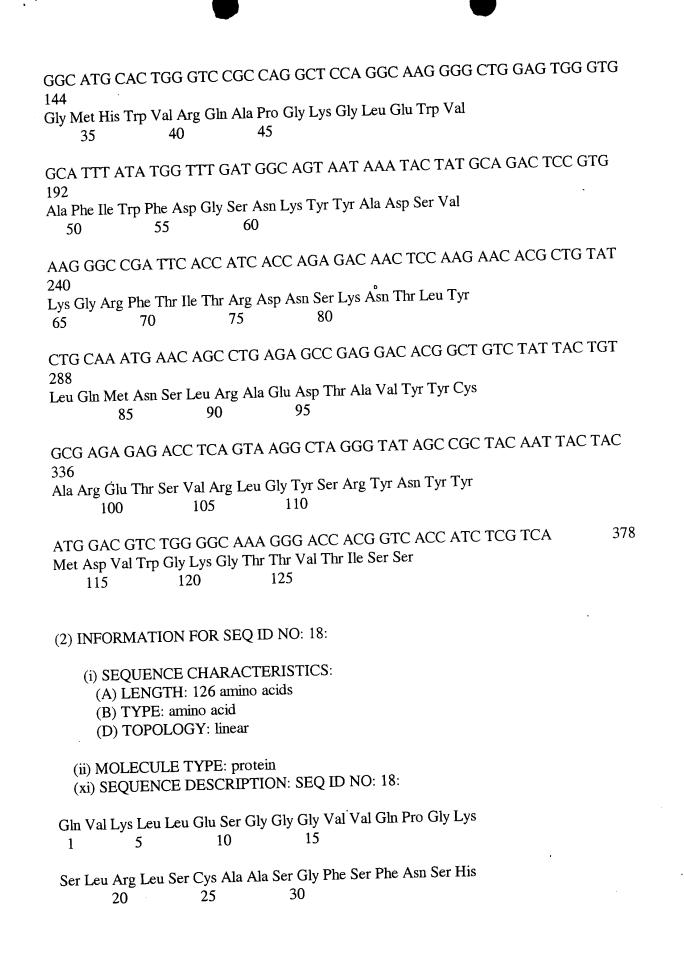
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Ser Ser Ser Ser Trp Thr Phe
85 90 95

Gly Gln Gly Thr Lys Val Glu Ile Lys 100 105

# (2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 378 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOL	ECULE TY	/PE: cDNA	to mRNA			
, ,	OTHETIC <i>A</i>					
. ,	I-SENSE:					
		YPE: N-ter	minal			
(vi) ORI	GINAL SO	URCE:				
		M: Homo sa	piens			
(C) I	NDIVIDU.	AL ISOLA	ГЕ: Hyperimmu	ine Rhesus D	donor	
(D) I	DEVELOP	MENTAL S	STAGE: adult			
	HAPLOTY					
(G) (	CELL TYP	E: Peripher	al lymphocyte E	3		
(vii) IMM	EDIATE S	SOURCE:				
			RARY, LD1			
(B) (	CLONE: LI	D1-117				
(viii) POS	ITION IN	GENOME:		1.4		
			MENT: Chrom	nosome 14		
(B)	MAP POSI	TION: q32.	.3 1 1	•		
(C)	JNITS: Ch	romosome	band number			
(ix) FEA						
	NAME/KE					
(B)	LOCATIO	N:13/8	ON./product=	"Immunaglal	ulin Fab"	
(D)	OTHER IN	IFORMATI	ION:/product=	Immunogiot	Jum, 1 ao	
(ix) FEA	ATURE:		CDDA CDDA			
(A)	NAME/KE	Y: CDR1, (	CDR2, CDR3	05 345)		
(B)	LOCATIO	N:jom(91)	105, 148198, 2	( <del>9</del> 33 <del>4</del> 3)		
(xi) SE	DUENCE I	DESCRIPT	ION: SEQ ID N	IO: 17:		
					G GTC CAG CCT GGG A	AG
48						
Gln Val L	ys Leu Leu		y Gly Gly Val V	al Gln Pro G	ly Lys	
1	5	10	15		•	
ፐርር ርፐር	AGA CTI	r TCC TGT	GCA GCG TO	CT GGA TTO	C AGT TTC AAT AGC CAT	Γ
Ser I en A	rg Len Ser	Cvs Ala Al	a Ser Gly Phe S	Ser Phe Asn S	er His	
	-6 -Cu Coi		30			



Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 40 35 Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val 60 55 50 Lys Gly Arg Phe Thr Ile Thr Arg Asp Asn Ser Lys Asn Thr Leu Tyr 75 70 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 90 85 Ala Arg Glu Thr Ser Val Arg Leu Gly Tyr Ser Arg Tyr Asn Tyr Tyr 110 105 100 Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Ile Ser Ser 125 120 115 (2) INFORMATION FOR SEQ ID NO: 19: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 318 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA LIBRARY, LD1 (B) CLONE: LD1-117

(viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: Chromosome 2 (B) MAP POSITION: p11 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..318 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(64..96, 142..162, 259..288) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19: GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 15 5 10 1 GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT AGG AGC CAT TTG AAT 96 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn 20 TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC TAT GCT Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala 45 40 35 GCA TCC AGT TTG CAA GGT GGG GTC CCA TCA AGG TTC AGT GGC AGT GGA Ala Ser Ser Leu Gln Gly Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 60 50 55 TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT GAA GAT 240 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 75 70 TTT GCA ACT TAT TAC TGT CAA CAG AGT TAC AGG GCC CCT CAG TGG ACG Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Ala Pro Gln Trp Thr

85 90 95

TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

318

### (2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 106 amino acids
  - (B) TYPE: amino acid(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg

1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn 20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala 35 40 45

Ala Ser Ser Leu Gln Gly Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Ala Pro Gln Trp Thr 85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 100 105

#### (2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 375 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA LIBRARY, LD2 (B) CLONE: LD2-1 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..375 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 295..342) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21: CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 1 5 10 15 TCC CTG AGA CTC TCC TGT GTA GCG TCT GGA TTC ACC CTC AGG AGT TAT 96 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr 30 25 20

GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGC CTG GAG TGG GTG Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 45 35 40 GCT TTT ATA TGG TTT GAT GGA AGT AAT AAA GGA TAT GTA GAC TCC GTG Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val 60 55 50 AAG GGC CGA TTC ACC ATC TCC CGA GAC AAT TCC AAG AAC ATG GTC TAT 240 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr 75 CTG CAA ATG AAC AGC CTG AGA GCC GAT GAC ACG GCT GTA TAT TAT TGT Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys 95 85 90 GCG AGA GAG AAG GCG CTT CGG GGA ATC AGC AGA TAC AAC TAT TAC CTG Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu 110 100 105 GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA 375 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 120 115 (2) INFORMATION FOR SEQ ID NO: 22: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22: Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 15 10 1 5

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr . 25 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 40 Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val 55 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr 75 Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys 90 Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu 105 110 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 120 (2) INFORMATION FOR SEQ ID NO: 23: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 333 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: Hyperimmund Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA LIBRARY, LD2 (B) CLONE: LD2-1
<ul> <li>(viii) POSITION IN GENOME:</li> <li>(A) CHROMOSOME/SEGMENT: chromosome 22</li> <li>(B) MAP POSITION: q11</li> <li>(C) UNITS: Chromosome band number</li> </ul>
<ul><li>(ix) FEATURE:</li><li>(A) NAME/KEY: CDS</li><li>(B) LOCATION:1333</li><li>(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"</li></ul>
(ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(6199, 145165, 262294)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:
GTG GTG ACT CAG CCA CCC TCA GCG TCT GGG ACC CCC GGA CAG AGG GTC 48  Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val  1 5 10 15
ACC ATC TCT TGT TCT GGA AGC AAC TCC ATC CTT GGA AGT AAG TAT GTA  96 Thr Ile Ser Cys Ser Gly Ser Asn Ser Ile Leu Gly Ser Lys Tyr Val  20 25 30
TAC TGG TAC CAG AAA CTC CCA GGA ACG GCC CCC AAA CTC CTC ATC TAT 144  Tyr Trp Tyr Gln Lys Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr 35 40 45
AAG AAT GAT CAG CGG CCC TCA GGG GTC TCT GAC CGA TTC TCT GGC TCC 192  Lys Asn Asp Gln Arg Pro Ser Gly Val Ser Asp Arg Phe Ser Gly Ser 50 55 60
AAG TCT GGC ACC TCG GCC TCC CTG GCC ATC AGT GGG CTC CGG TCC GAG 240  Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg Ser Glu 65 70 75 80

GAT GAG GCT GAC TAT TAC TGT GCA CCA TGG GAT GCC AAC CTG GGT GGC 288 Asp Glu Ala Asp Tyr Tyr Cys Ala Pro Trp Asp Ala Asn Leu Gly Gly 90 95 CCG GTG TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA AGT CAG CCC 333 Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro 100 105 110 (2) INFORMATION FOR SEQ ID NO: 24: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 111 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24: Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val 15 10 1 5 Thr Ile Ser Cys Ser Gly Ser Asn Ser Ile Leu Gly Ser Lys Tyr Val 20 25 30 Tyr Trp Tyr Gln Lys Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr 40 45 35 Lys Asn Asp Gln Arg Pro Ser Gly Val Ser Asp Arg Phe Ser Gly Ser 60 50 55 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg Ser Glu 80 65 70 75 Asp Glu Ala Asp Tyr Tyr Cys Ala Pro Trp Asp Ala Asn Leu Gly Gly 85 90 95 Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro 105 110 100 (2) INFORMATION FOR SEQ ID NO: 25: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 375 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: homo sapiens (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA Library, LD2 (B) CLONE: LD2-4 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..375 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION: join(91..105, 148..198, 295..342) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25: CAG GTG AAA CTG CTC GAG TCG GGG GGA GGC GTG GTC CAG CCG GGG GGG Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 10 15

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TCC CTG AGA CTC TCC TGT GAA GCG TCT GGA TTC ACC CTC AGA AGT TCT 96 Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser 30 25 20 GGC ATG CAC TGG GTC CGC CAG GCT CCT GGC AAG GGG CTG GAG TGG GTG Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 45 40 35 GCA CTT ATA TGG TTT GAT GGA AGT ATC AGA TCG TAT GCA GAA TCC GTG 192 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val 60 55 AAG GGC CGA TTC ACC ATC TCC AGA GAC ACT TCC AAG AAC ACC CTA TAT Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr 80 75 70 65 CTC CAA ATG CGC AGT CTG AGT GCC GAC GAC ACG GCT GTG TAT TAC TGT Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys 90 95 85 GCG AGA GAC AAG GCG GTT CGG GGA ATT AGC AGG TAC AAC TAT TAC ATG 336 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 110 105 100 GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA 375 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 115 120 (2) INFORMATION FOR SEQ ID NO: 26: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 1 5 10 15
Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser 20 25 30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45
Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val 50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr 65 70 75 80
Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys 85 90 95
Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 100 105 110
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120 125
(2) INFORMATION FOR SEQ ID NO: 27:
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 312 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>
(ii) MOLECULE TYPE: cDNA to mRNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(v) FRAGMENT TYPE: N-terminal
<ul> <li>(vi) ORIGINAL SOURCE:</li> <li>(A) ORGANISM: Homo sapiens</li> <li>(C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor</li> <li>(D) DEVELOPMENTAL STAGE: adult</li> <li>(E) HAPLOTYPE: diploid</li> </ul>

(G) CELL TYPE: Peripheral lymphocyte B
(vii) IMMEDIATE SOURCE:  (A) LIBRARY: cDNA library, LD2  (B) CLONE: LD2-4
(viii) POSITION IN GENOME:  (A) CHROMOSOME/SEGMENT: chromosome 2  (B) MAP POSITION: p11  (C) UNITS: Chromosome band number
<ul> <li>(ix) FEATURE:</li> <li>(A) NAME/KEY: CDS</li> <li>(B) LOCATION:1312</li> <li>(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"</li> </ul>
(ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(6496, 142162, 259282)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:
GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 1 5 10 15
GTC ACC ATC ACT TGC CGG ACA AGT CAG ACC ATT AGC AGA AAT TTA AAT
96 Val Thr Ile Thr Cys Arg Thr Ser Gln Thr Ile Ser Arg Asn Leu Asn 20 25 30
TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC TAT GCT
144 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala 35 40 45
ACA TCC AGT TTG CAA AGT GGG GTC CCA TCA AGG TTC AGT GGC AGT GGA
<ul> <li>192</li> <li>Thr Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly</li> <li>50</li> <li>55</li> <li>60</li> </ul>
TCT GGG ACA GAT TTC ACT CTC ACC ATC AAT AGT CTA CAA CCT GAA GAT 240

. 3

Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp 65 75 TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC ACT ACC CCT TCG TTC GGC Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Ser Phe Gly 90 95 85 312 CAA GGG ACC AAG GTG GAA ATC AAA Gln Gly Thr Lys Val Glu Ile Lys 100 (2) INFORMATION FOR SEQ ID NO: 28: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 104 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28: Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 15 5 10 Val Thr Ile Thr Cys Arg Thr Ser Gln Thr Ile Ser Arg Asn Leu Asn 25 30 20 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala 45 35 40 Thr Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 60 55 50 Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp 75 80 70 65 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Ser Phe Gly 90 95 85 Gln Gly Thr Lys Val Glu Ile Lys 100 (2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 375 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: homo sapiens
  - (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
  - (D) DEVELOPMENTAL STAGE: adult
  - (E) HAPLOTYPE: diploid
  - (G) CELL TYPE: Peripheral lymphocyte B
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA library, LD2
  - (B) CLONE: LD2-4
- (viii) POSITION IN GENOME:
  - (A) CHROMOSOME/SEGMENT: chromosome 2
  - (B) MAP POSITION: p11
  - (C) UNITS: Chromosome band number
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..375
  - (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"
- (ix) FEATURE:
  - (A) NAME/KEY: CDR1, CDR2, CDR3
  - (B) LOCATION:join(91..105, 148..198, 295..342)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC TTG GTC CAG CCG GGG GGG 48

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

			G TCT GGA TTC ACC TTC AGG AGT TAT he Thr Phe Arg Ser Tyr	96
GGC ATG CAC	TGG GTC CG	GC CAG GC	T CCA GGC AAG GGC CTG GAG TGG GTG	
	Val Arg Gln A 40	la Pro Gly L 45	ys Gly Leu Glu Trp Val	
GCT TTT ATA 192	TGG TTT GA	T GGA AGT	T AAT AAA GGA TAT GTA GAC TCC GTG	
	• •	r Asn Lys Gl 60	ly Tyr Val Asp Ser Val	
AAG GGC CGA	A TTC ACC AT	C TCC CGA	A GAC AAT TCC AAG AAC ATG CTC TAT	
			er Lys Asn Met Leu Tyr 80	
CTG CAA ATG	AAT AGC CT	G AGA GC	C GAG GAC ACG GCT GTA TAT TAT TGT	
	n Ser Leu Arg A	Ala Glu Asp 95	Thr Ala Val Tyr Tyr Cys	
GCG AGA GAO	G AAG GCG C	TT CGG GC	GA ATC AGT AGA TAC AAC TAT TAC CTG	
	s Ala Leu Arg C 105	Gly Ile Ser Ai 110	rg Tyr Asn Tyr Tyr Leu	
Asp Val Trp Gly		hr Val Thr V	CG GTC ACC GTC TCC TCA 375 Val Ser Ser	
(2) INFORMAT	TION FOR SEC	) ID NO: 30:	:	
(A) LENG (B) TYPE	NCE CHARAC GTH: 125 amin B: amino acid DLOGY: linear		<b>:</b>	
	JLE TYPE: pro ICE DESCRIP		ID NO: 30:	

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly 1 5 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr 25 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val 60 55 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Leu Tyr 70 75 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu 110 105 Asp Val Trp Gly Lys Gly Ala Thr Val Thr Val Ser Ser 125 120 (2) INFORMATION FOR SEQ ID NO: 31: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 318 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B

(A) LIBRARY: cDND library. LD2 (B) CLONE: LD2-5
<ul> <li>(viii) POSITION IN GENOME:</li> <li>(A) CHROMOSOME/SEGMENT: chromosome 2</li> <li>(B) MAP POSITION: p11</li> <li>(C) UNITS: Chromosome band number</li> </ul>
<ul><li>(ix) FEATURE:</li><li>(A) NAME/KEY: CDS</li><li>(B) LOCATION:1318</li><li>(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"</li></ul>
(ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(6496, 142162, 259288)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:
GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT ATA GGC GAC AGA
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg  1 5 10 15
GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC GTT ACC AGG TCT TTA AAT 96
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Thr Arg Ser Leu Asn 20 25 30
TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AGG CTC CTA ATC TTT GCT 144
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Phe Ala 35 40 45
GCG TCC ACT TTG CAA AGT GGG GTC CCA TCA AGG TTC AGT GGC AGT GGA 192
Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60
TCT GGG ACA GAT TTC ACC CTC ACC ATC AGC AGT CTG CAA CCT GAG GAT 240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 65 70 75 80

(vii) IMMEDIATE SOURCE:

TTT GGA ACT TAC TGT CAA CAG AAT TAC AGG ACC CCT CAG TGG ACG 288 Phe Gly Thr Tyr Tyr Cys Gln Gln Asn Tyr Arg Thr Pro Gln Trp Thr 90 95 85 TTC GGC CAA GGG ACC AAG GTA GAA ATC AAA 318 Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 100 105 (2) INFORMATION FOR SEQ ID NO: 32: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 106 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32: Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg 1 5 10 15 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Thr Arg Ser Leu Asn 30 20 25 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Phe Ala 40 45 35 Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 80 65 70 75 Phe Gly Thr Tyr Tyr Cys Gln Gln Asn Tyr Arg Thr Pro Gln Trp Thr 90 95 85 Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 100 105 (2) INFORMATION FOR SEQ ID NO: 33: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 378 base pairs

- (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD2 (B) CLONE: LD2-10 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..378 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 298..345) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:
- CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG 48
  Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
  1 5 10 15

TCC CTG AGA CTC TCC TGT GTA GCG TCT GGA TTC ACC CTC AGG AGT TAT Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr 20 25 30
GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGC CTG GAG TGG GTG 144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45
GCT TTT ATA TGG TTT GAT GGA AGT AAT AAA GGA TAT GTA GAC TCC GTG 192
Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val 50 55 60
AAG GGC CGA TTC ACC ATC TCC CGA GAC AAT TCC AAG AAC ATG GTC TAT 240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr 175 180 185
CTG CAA ATG AAC AGC CTG AGA GCC GAT GAC ACG GCT GTA TAT TAT 288
Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr 85 90 95
TGT GCG AGA GAG AAG GCG CTT CGG GGA ATC AGC AGA TAC AAC TAT TAC 336
Cys Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr 100 105 110
CTG GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA  Leu Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  115 120 125
(2) INFORMATION FOR SEQ ID NO: 34:
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 126 amino acids</li><li>(B) TYPE: amino acid</li><li>(D) TOPOLOGY: linear</li></ul>
(ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Gln Val Lys Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly

1	5		10	15	5
Ser Le	u Arg Le 20	u Ser Cya 25		Ser Gly 30	Phe Thr Leu Arg Ser Tyr
•	et His Trp 35	p Val Arg 40	g Gln Ala	Pro Gly 45	y Lys Gly Leu Glu Trp Val
Ala Ph 50	ne Ile Trp	Phe Asp 55	Gly Ser A	•	Gly Tyr Val Asp Ser Val
Lys Gl 65		e Thr Ile 70	Ser Arg 75	Asp Asn	n Ser Lys Asn Met Val Tyr 80
Leu G	ln Met As 85	sn Ser Le	u Arg Al 90	a Asp As 95	sp Thr Ala Val Tyr Tyr Tyr 5
Cys Al	la Arg Glo 100	u Lys Ala 10	_	g Gly Ile 110	Ser Arg Tyr Asn Tyr Tyr
	sp Val Tr 15	p Gly Ly 120	s Gly Thr	Thr Va	al Thr Val Ser Ser
(2) IN	FORMAT	ΓΙΟΝ FO	R SEQ I	D NO: 3	35:
.,	SEQUEN (A) LEN (B) TYPI (C) STRA (D) TOP	GTH: 33 E: nucleid ANDEDI	3 base pa cacid NESS: sir	irs	S:
(ii) l	MOLECU	JLE TYF	PE: cDNA	A to mR	NA
(iii)	НҮРОТЕ	IETICAL	.: NO		
(iv)	ANTI-SI	ENSE: N	0		
(v)	FRAGM	ENT TY	PE: N-te	rminal	
` , ,	ORIGIN (A) ORG (C) INDI (D) DEV (E) HAPI (G) CELI	ANISM: VIDUAI ELOPM LOTYPE	Homo sa L ISOLA ENTAL S E: diploid	TE: hype STAGE:	

(vii) IMMEDIATE SOURCE:  (A) LIBRARY: cDNA library, LD2  (B) CLONE: LD2-10
(viii) POSITION IN GENOME:  (A) CHROMOSOME/SEGMENT: chromosome 22  (B) MAP POSITION: q11  (C) UNITS: Chromosome band number
<ul><li>(ix) FEATURE:</li><li>(A) NAME/KEY: CDS</li><li>(B) LOCATION:1333</li><li>(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"</li></ul>
(ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(61102, 148168, 265294)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:
GTG GTG ACT CAG GAG CCC TCA CTG ACT GTG TCC CCA GGA GGG ACA GTC
Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val 1 5 10 15
ACT CTC ACC TGT GCT TCC AGC ACT GGG GCA GTC ACC AGG GGT TAC TAT
Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Arg Gly Tyr Tyr 20 25 30
CCA AAC TGG TTC CAG CAG AAG CCT GGA CAA GCA CCC AGG GCA CTG ATT 144
Pro Asn Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Ala Leu Ile 35 40 45
TAT AGT ACA AAC AAA AAA CAC TCC TGG ACC CCT GCC CGG TTC TCA GGC 192
Tyr Ser Thr Asn Lys Lys His Ser Trp Thr Pro Ala Arg Phe Ser Gly 50 55 60
TCC CTC CTT GGG GGC AAA GCT GCC CTG ACA CTG TCA GGT GTG CAG CCT 240
Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro 65 70 75 80

GAA GAC GAG GCT GAA TAT TAC TGC CTG CTC TAC TAT GGT GGT GCT CAA 288 Glu Asp Glu Ala Glu Tyr Tyr Cys Leu Leu Tyr Tyr Gly Gly Ala Gln 90 95 85 CTC GTA TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA CGT CAG CCC 333 Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Arg Gln Pro 110 105 100 (2) INFORMATION FOR SEQ ID NO: 36: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 111 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36: Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val 15 10 1 5 Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Arg Gly Tyr Tyr 30 20 25 Pro Asn Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Ala Leu Ile 40 45 35 Tyr Ser Thr Asn Lys Lys His Ser Trp Thr Pro Ala Arg Phe Ser Gly 60 55 50 Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro 80 70 75 65 Glu Asp Glu Ala Glu Tyr Tyr Cys Leu Leu Tyr Tyr Gly Gly Ala Gln 95 90 85 Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Arg Gln Pro 110 105 100 (2) INFORMATION FOR SEQ ID NO: 37: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 375 base pairs

- (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD2 (B) CLONE: LD2-11 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..375 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 295..342)
- CAG GTG AAA CTG CTC GAG TCG GGG GGA GGC GTG GTC CAG CCG GGG GGG 48 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

TCC CTG AGA CTC TCC TGT GAA GCG TCT GGA TTC ACC CTC AGA AGT TCT Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser 30 20 25 GGC ATG CAC TGG GTC CGC CAG GCT CCT GGC AAG GGG CTG GAG TGG GTG Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 40 45 35 GCA CTT ATA TGG TTT GAT GGA AGT ATC AGA TCG TAT GCA GAA TCC GTG 192 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val 55 AAG GGC CGA TTC ACC ATC TCC AGA GAC ACT TCC AAG AAC ACC CTA TAT Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr 70 75 80 CTC CAA ATG CGC AGT CTG AGT GCC GAC GAC ACG GCT GTG TAT TAC TGT Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys 90 95 85 GCG AGA GAC AAG GCG GTT CGG GGA ATT AGC AGG TAC AAC TAT TAC ATG 336 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 100 105 110 375 GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120 125 (2) INFORMATION FOR SEQ ID NO: 38: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 amino acids (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

·	
Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 1 5 10 15	
Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser 20 25 30	•
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Va 35 40 45	l
Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val 50 55 60	
Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr 65 70 75 80	
Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cy 85 90 95	'S
Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 100 105 110	
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120 125	
(2) INFORMATION FOR SEQ ID NO: 39:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 315 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA to mRNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: N-terminal	
<ul> <li>(vi) ORIGINAL SOURCE:</li> <li>(A) ORGANISM: Homo sapiens</li> <li>(C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D dono</li> <li>(D) DEVELOPMENTAL STAGE: adult</li> <li>(E) HAPLOTYPE: diploid</li> </ul>	r

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(G) CELL TYPE: lymphocvyte
<ul><li>(vii) IMMEDIATE SOURCE:</li><li>(A) LIBRARY: cDNA library, LD2</li><li>(B) CLONE: LD2-11</li></ul>
<ul> <li>(viii) POSITION IN GENOME:</li> <li>(A) CHROMOSOME/SEGMENT: chromosome 2</li> <li>(B) MAP POSITION: p11</li> <li>(C) UNITS: Chromosome band number</li> </ul>
<ul> <li>(ix) FEATURE:</li> <li>(A) NAME/KEY: CDS</li> <li>(B) LOCATION:1315</li> <li>(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"</li> </ul>
(ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(6496, 142162, 259285)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:
GTG TTG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT ATA CGA GAC AGA
48 Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Arg Asp Arg 1 5 10 15
GTC ACC ATC ACT TGC CGG GCA AGT CAG AAC ATT GGC AGT TAT TTA AAT
96 Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Gly Ser Tyr Leu Asn 20 25 30
TGG TAT CAG CAC AAA CCA GGG ACA GCC CCT AAA CTC CTG ATC TAT GCT
144 Trp Tyr Gln His Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala 35 40 45
GTA TCC GCT TTG CAA AGT GGG GTC CCA TCG AGG TTC AGT GGC AGT AGA
<ul> <li>192</li> <li>Val Ser Ala Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg</li> <li>50</li> <li>55</li> <li>60</li> </ul>
TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT GAA GAT 240

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Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 70 75 TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC AGT CCC CCG TAC ACT TTC Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Pro Pro Tyr Thr Phe 95 90 85 GGC CAG GGG ACC AAC CTG CAG ATC AAA 315 Gly Gln Gly Thr Asn Leu Gln Ile Lys 100 105 (2) INFORMATION FOR SEQ ID NO: 40: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40: Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Arg Asp Arg 10 15 5 Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Gly Ser Tyr Leu Asn 30 20 25 Trp Tyr Gln His Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala 35 40 45 Val Ser Ala Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg 50 55 60 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 70 75 80 65 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Pro Pro Tyr Thr Phe 85 90 95 Gly Gln Gly Thr Asn Leu Gln Ile Lys 105 100 (2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 375 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD2 (B) CLONE: LD2-14 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 14 (B) MAP POSITION: q32.3 (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..375 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 295..342) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41: CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 1 5 10

			TCT GGA TTC ACC TTC AC e Thr Phe Arg Asn Phe	G AAT TIT
GGC ATG C	AC TGG GTC (	CGC CAG GCT	r CCA GGC AAG GGG CTG C	GAG TGG GTG
144				
Gly Met His 7	Trp Val Arg Gln 40	Ala Pro Gly Ly 45	ys Gly Leu Glu Trp Val	
GCT TTT AT	IT TGG TTT G	AT GCA AGT	AAT AAA GGA TAT GGA GA	AC TCC GTT
	rp Phe Asp Ala S 55	Ser Asn Lys Gly 60	y Tyr Gly Asp Ser Val	
AAG GGC C	CGA TTC ACC	GTC TCC AGA	A GAC AAT TCC AAG AAC A	CG CTC TAT
		Arg Asp Asn S 75 8	er Lys Asn Thr Leu Tyr 0	
CTG CAA A	TG AAC GGC	CTG AGA GC	C GAA GAC ACG GCT GTA T	TAT TAT TGT
	•	g Ala Glu Asp' 95	Thr Ala Val Tyr Tyr Cys	
GCG AGA G	GAG AAG GCG	GTT CGG GG	A ATT AGT AGA TAC AAC	TAC TAC ATG
	Lys Ala Val Arg 105	Gly Ile Ser Arg	g Tyr Asn Tyr Tyr Met	
	GG GGC AAG Gly Lys Gly Thr 120		G GTC ACC GTC TCC TCA al Ser Ser	375
(2) INFORM	ATION FOR SI	EQ ID NO: 42:		
` '	UENCE CHARA ENGTH: 125 am			
` '	PE: amino acid	may waster		
` '	OPOLOGY: line	ar		
	CULE TYPE: p		D NO. 42.	
(x1) SEQU	ENCE DESCRI	RTION: SEQ I	D NO: 42:	

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly

1	5		10	15	
Ser Le	eu Arg Va 20	al Ala Cys 25		Ser Gly Pl 30	he Thr Phe Arg Asn Phe
•	let His Tr 35	p Val Arg 40		Pro Gly L 45	ys Gly Leu Glu Trp Val
Ala Pl 50	ne Ile Trp	Phe Asp 55	Ala Ser A	-	ly Tyr Gly Asp Ser Val
Lys G 65	• -	e Thr Va 70	l Ser Arg 75	-	Ser Lys Asn Thr Leu Tyr 80
Leu G	In Met A	sn Gly Le	eu Arg Ala 90	a Glu Asp 95	Thr Ala Val Tyr Tyr Cys
Ala A	rg Glu Ly 100		l Arg Gly )5	Ile Ser Ar 110	rg Tyr Asn Tyr Tyr Met
	al Trp Gl l 15	y Lys Gly 120	y Thr Thr	Val Thr V 125	Val Ser Ser
(2) IN	FORMA'	TION FC	R SEQ II	O NO: 43:	
(i)	(A) LEN (B) TYP (C) STR	GTH: 31 E: nuclei	NESS: sin	irs	•
(ii)	MOLEC	ULE TYI	PE: cDNA	to mRN	A
(iii)	НҮРОТЬ	IETICAI	L: NO		
(iv)	ANTI-S	ENSE: N	О		
(v)	FRAGM	ENT TY	PE: N-ter	minal	
(vi)	(C) INDI (D) DEV (E) HAP	SANISM: IVIDUAI ELOPM LOTYPE	Homo sa	ΓE: hyperi STAGE: a	immune Rhesus D donor dult

(vii) IMMEDIATE SOURCE:  (A) LIBRARY: cDNA library, LD2  (B) CLONE: LD2-14
(viii) POSITION IN GENOME:  (A) CHROMOSOME/SEGMENT: chromosome 2  (B) MAP POSITION: p11  (C) UNITS: Chromosome band number
<ul><li>(ix) FEATURE:</li><li>(A) NAME/KEY: CDS</li><li>(B) LOCATION:1315</li><li>(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"</li></ul>
(ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(6496, 142162, 259285)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:
GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTG GGA GAC AGA
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 1 5 10 15
GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT ATC AAC AAT TTA AAT 06 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Asn Asn Leu Asn
20 25 30
TGG TAT CAG CAG AAA CCA GGC AAA GCC CCT GAA CTC CTG ATC TAT GCT
Frp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile Tyr Ala 35 40 45
GCA TCC AGT TTG CAA AGT GGG GTC CCT TCA AGG TTC CGT GGC AGT GGA
Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Arg Gly Ser Gly 50 55 60
TCT GGG AGA GAT TTC ACT CTC ACC GTC ACC AGT CTG CAA CCT GAA GAT
240 Ser Gly Arg Asp Phe Thr Leu Thr Val Thr Ser Leu Gln Pro Glu Asp 65 70 75 80

TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC AGT ACC CTG TGG ACG TTC 288 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Trp Thr Phe 90 85 95 GGC CAA GGG ACC AAG GTG GAA ATC AAA 315 Gly Gln Gly Thr Lys Val Glu Ile Lys 100 (2) INFORMATION FOR SEQ ID NO: 44: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44: Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 1 5 10 15 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Asn Asn Leu Asn 20 25 30 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile Tyr Ala 45 35 40 Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Arg Gly Ser Gly 50 55 Ser Gly Arg Asp Phe Thr Leu Thr Val Thr Ser Leu Gln Pro Glu Asp 65 70 75 80 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Trp Thr Phe 85 90 95 Gly Gln Gly Thr Lys Val Glu Ile Lys 100 105 (2) INFORMATION FOR SEQ ID NO: 45: (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 375 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA llibrary (B) CLONE: LD2-17 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 14 (B) MAP POSITION: q32.43 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..375 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 295..342) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45: CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG 48 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 15 1 5 10

		CTC TCC T Ser Cys Val 25						AGG AGT	TAT
GGC A'	TG CAC	TGG GTC (	CGC C	AG GCT	CCA G	GC AAG	GGC CT	G GAG TO	G GTG
		Val Arg Gln 40	Ala Pr 45		Gly Le	u Glu TrŢ	Val		
GCT T.	TT ATA	rgg ttt e	SAT GO	GA AGT A	AAT AA	A GGA	TAT GTA	A GAC TCC	CGTG
	: Ile Trp P	the Asp Gly 55	Ser Ası 60	n Lys Gly	Tyr Val	Asp Ser	Val		
AAG G 240	GC CGA	TTC ACC	ATC TO	CC CGA	GAC A	AT TCC	AAG AA	C ACG CT	C TAT
	Arg Phe	Thr Ile Ser .	Arg As <sub>l</sub> 75	p Asn Ser 80		n Thr Lei	ı Tyr	·	
288		AAG AGC Ser Leu Ar						ΓΑ ΤΑΤ ΤΑ	AT TGT
Leu Gii	85	90	g Ala O	95	ш Ала У	ai Tyi Ty	n Cys		
GCG A	GA GAG	AAG GCG	CTT C	CGG GGA	A ATC A	AGT AGA	A TAC A	AC TAT TA	AC CTG
	g Glu Lys 100	Ala Leu Arg 105	g Gly Il	e Ser Arg 110	Tyr Ası	n Tyr Tyr	Leu		
Asp Va	ıl Trp Gly	GGC AAG Lys Gly Th 120	r Thr V				C TCC TC	CA	375
(2) INF	FORMAT	ION FOR S	EQ ID	NO: 46:					
(	(A) LENC (B) TYPE	NCE CHARA GTH: 125 and acid CLOGY: line	nino aci I						
		LE TYPE: <sub>I</sub> CE DESCR		N: SEQ II	) NO: 4	6:			

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly

5	10	15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45

Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 65 70 75 80

Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95

Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu 100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120 125

## (2) INFORMATION FOR SEQ ID NO: 47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 315 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
  - (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
  - (D) DEVELOPMENTAL STAGE: adult
  - (E) HAPLOTYPE: diploid
  - (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:  (A) LIBRARY: cDNA library, LD2  (B) CLONE: LD2-17
(viii) POSITION IN GENOME:  (A) CHROMOSOME/SEGMENT: chromosome 2  (B) MAP POSITION: p11  (C) UNITS: Chromosome band number
<ul><li>(ix) FEATURE:</li><li>(A) NAME/KEY: CDS</li><li>(B) LOCATION:1315</li><li>(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"</li></ul>
(ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(6496, 142162, 259285)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:
GTG ATG ACC CAG TCT CCA TTC TCC CTG TCT GCA TCT GTA GGA GAC AGA
Val Met Thr Gln Ser Pro Phe Ser Leu Ser Ala Ser Val Gly Asp Arg 1 5 10 15
GTC ACC ATC ACT TGC CGG GCA AGT CAG AAC ATT AGG AGT TTT TTA AGT 96
Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Arg Ser Phe Leu Ser 20 25 30
TGG TAT CAG CAG AAA CCA GGG ACA GCC CCT AAG CTC CTG ATC TAT GCT
Trp Tyr Gln Gln Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala 35 40 45
GCA TCC AGG TTG CAA AGT GGG GTC CCA TCA AGG TTC AGT GGC AGT GGG 192
Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60
TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC ACT CTG CAA CCT GAA GAT 240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Leu Gln Pro Glu Asp 65 70 75 80

TTT GCG ACT TAC TGT CAA CAG AGT TAC AGT GCC CCT TGG ACG TTC Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ala Pro Trp Thr Phe 90 95 85 315 GGC CAA GGG ACC AAG CTG GAA ATC AAA Gly Gln Gly Thr Lys Leu Glu Ile Lys 100 105 (2) INFORMATION FOR SEQ ID NO: 48: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48: Val Met Thr Gln Ser Pro Phe Ser Leu Ser Ala Ser Val Gly Asp Arg 5 10 15 Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Arg Ser Phe Leu Ser 30 25 20 Trp Tyr Gln Gln Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala 40 45 35 Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 55 60 50 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Leu Gln Pro Glu Asp 70 75 80 65 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ala Pro Trp Thr Phe 90 95 85 Gly Gln Gly Thr Lys Leu Glu Ile Lys 100 105 (2) INFORMATION FOR SEQ ID NO: 49: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 375 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library LD2 (B) CLONE: LD2-20 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..375 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 295..342) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49: CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 10 15

										CAGG	AGT TAT	
Ser Let	ı Arg Let	ı Ser (		Ala Se		e Thr S	Ser Ar	g Ser T	`yr			
	20		25		30							
	TG CAC	TGG	GTC C	GC C	AG GCT	CCA	GGC.	AAG (	GGC CI	ΓG GA	G TGG GT	Ġ.
144 Cly Ma	et His Trp	. Wal	Ara Gln	Δla Pr	o Gly I v	s Glv l	Len Gl	lu Tro	Val			
50	.c 1115 11 <sub>1</sub>	55	ag Om z	60	oʻoty 12)	s Oly	20u 01	u IIp				
GCT T 192	ТТ АТА	TGG	TTT GA	AT GO	GA AGT	AAT .	AAA (	GGA T	AT GT	A GAC	TCC GTG	j
	e Ile Trp 7		sp Gly S 7	_	n Lys Gly 80		/al Asp	Ser V	'al			
AAG (	GGC CGA	A TTC	C ACC A	TC T	CC CGA	GAC	AAT	TCC A	AG AA	C AC	G CTC TAT	Γ
	y Arg Phe 85	e Thr 1	le Ser A 90	rg As	p Asn Se 95	r Lys A	Asn Th	r Leu '	Гуг			
CTG C 288	CAA ATO	S AAC	G AGC C	TG A	GA GC0	C GAG	GAC	ACG	GCT G	ТА ТА	T TAT TG	T
	n Met Ly 100	s Ser	Leu Arg 105	Ala G	ilu Asp T 110	hr Ala	Val T	`yr Tyr	Cys			
GCG A	AGA GA	G AA	G GCG (	CTT (	CGG GG	A ATO	CAGT	`AGA	TAC A	AC TA	AT TAC CT	'G
	g Glu Lys 205	s Ala l	Leu Arg 210	Gly Il	e Ser Arg 215	g Tyr A	Asn Ty	r Tyr I	æu			
	GTC TG( al Trp Gl							GTC	TCC T(	CA	375	5
(2) IN	FORMAT	ΓΙΟΝ	FOR SE	Q ID	NO: 50:							
,,	SEQUE (A) LENG (B) TYPI	GTH: E: ami	125 ami no acid	no aci								
(ii) l	(D) TOP MOLECU SEQUEN	JLE T	YPE: pr	otein	N: SEQ I	D NO:	: 50:					

Gln Val Lys Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly

1	5	10	1	15		
Ser Leu	Arg Leu 20	Ser Cys Val	Ala Ser G 30	ly Phe Thr Ser A	Arg Ser Tyr	
Gly Met	_	Val Arg Gln 40	Ala Pro G 45	ly Lys Gly Leu	Glu Trp Val	
Ala Phe 50	Ile Trp F	Phe Asp Gly S 55	er Asn Ly 60	rs Gly Tyr Val A	Asp Ser Val	
Lys Gly 65	Arg Phe			sn Ser Lys Asn 80	Thr Leu Tyr	
Leu Gln	Met Lys 85	Ser Leu Arg 90		Asp Thr Ala Val 95	l Tyr Tyr Cys	
_	Glu Lys 100	Ala Leu Arg 105	Gly Ile Se 11	r Arg Tyr Asn ' 0	Гуг Туг Leu	
Asp Val		Lys Gly Thr	Thr Val T 125	hr Val Ser Ser		
(2) INF	ORMAT	ION FOR SE	Q ID NO:	51:		
() () ()	A) LENG B) TYPE C) STRA	CE CHARAC TH: 315 base: nucleic acid NDEDNESS DLOGY: linea	e pairs : single	CS:		
(ii) M	OLECU	LE TYPE: cI	ONA to m	RNA		
(iii) H	YPOTHI	ETICAL: NO				
(iv) A	ANTI-SE	NSE: NO				
(v) <b>F</b>	FRAGME	ENT TYPE: N	I-terminal			
() () ()	A) ORGA C) INDIV D) DEVE E) HAPL	AL SOURCE: ANISM: Hom VIDUAL ISO ELOPMENTA OTYPE: dipl TYPE: Perir	LATE: hy AL STAG oid		esus D donor	

(vii) IMMEDIATE SOURCE:  (A) LIBRARY: cDNA library, LD2  (B) CLONE: LD2-20
(viii) POSITION IN GENOME:  (A) CHROMOSOME/SEGMENT: chromosome 2  (B) MAP POSITION: p11  (C) UNITS: Chromosome band number
<ul><li>(ix) FEATURE:</li><li>(A) NAME/KEY: CDS</li><li>(B) LOCATION:1315</li><li>(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"</li></ul>
(ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(6496, 142162, 259285)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:
GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  1 5 10 15
GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT AGC AGC TAT TTA AAT
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn 20 25 30
TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC TAT GCT
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala 35 40 45
GCA TCC AGT TTG CAA AGT GGG GTC CCA TCA AGG TTC AGT GGC AGT GGA 192
Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60
TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT GAA GAT 240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 65 70 75 80

TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC AGT ACC CGA TTC ACT TTC 288 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Arg Phe Thr Phe 90 95 85 315 GGC CCT GGG ACC AAA GTG GAT ATC AAA Gly Pro Gly Thr Lys Val Asp Ile Lys 100 105 (2) INFORMATION FOR SEQ ID NO: 52: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52: Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 10 15 5 1 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn 30 25 20 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala 45 40 35 Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 60 50 55 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 75 80 70 65 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Arg Phe Thr Phe 90 95 85 Gly Pro Gly Thr Lys Val Asp Ile Lys 105 100 (2) INFORMATION FOR SEQ ID NO: 53: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 384 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD1 (B) CLONE: LD1-6-17 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..384 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 295..351) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53: CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG 48 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg 5 10 15

TCC CTG AGA CTT TCC TGT GCA GCG TCT GGA TTT ACC TTC AGT AGC TAT Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr 30 25 20 GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG 144 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 45 35 GCA GAT ATA TGG TTT GAT GGA GGT AAT AAA CAT TAT GCA GAC TTC GTG Ala Asp Ile Trp Phe Asp Gly Gly Asn Lys His Tyr Ala Asp Phe Val 55 60 50 AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC ACG GTG TAT Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr 80 65 70 75 CTA CAA ATG AAC AGC CTG AGA GTC GAG GAC ACG GCT GTG TAT TAC TGT 288 Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys 90 85 GCG AGG GAT TAC TAT AGC GTT ACT AAG AAA CTC AGA CTC CAC TAC TAC 336 Ala Arg Asp Tyr Tyr Ser Val Thr Lys Lys Leu Arg Leu His Tyr Tyr 110 105 100 TAC TAC ATG GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA 384 Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 230 225 220 (2) INFORMATION FOR SEQ ID NO: 54: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 128 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg  1 5 10 15  Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr 20 25 30  Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45  Ala Asp Ile Trp Phe Asp Gly Gly Asn Lys His Tyr Ala Asp Phe Val 50 55 60  Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr 65 70 75 80  Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95  Ala Arg Asp Tyr Tyr Ser Val Thr Lys Lys Leu Arg Leu His Tyr Tyr 100 105 110  Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120 125  (2) INFORMATION FOR SEQ ID NO: 55:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA to mRNA  (iii) HYPOTHETICAL: NO  (iv) ANTI-SENSE: NO  (v) FRAGMENT TYPE: N-terminal  (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult	·
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35	- 40
Ala Asp Ile Trp Phe Asp Gly Gly Asn Lys His Tyr Ala Asp Phe Val 50 55 60  Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr 65 70 75 80  Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95  Ala Arg Asp Tyr Tyr Ser Val Thr Lys Lys Leu Arg Leu His Tyr Tyr 100 105 110  Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120 125  (2) INFORMATION FOR SEQ ID NO: 55:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA to mRNA  (iii) HYPOTHETICAL: NO  (v) FRAGMENT TYPE: N-terminal  (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor	
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr 65 70 75 80  Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95  Ala Arg Asp Tyr Tyr Ser Val Thr Lys Lys Leu Arg Leu His Tyr Tyr 100 105 110  Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120 125  (2) INFORMATION FOR SEQ ID NO: 55:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA to mRNA  (iii) HYPOTHETICAL: NO  (iv) ANTI-SENSE: NO  (v) FRAGMENT TYPE: N-terminal  (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor	· ·
Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95  Ala Arg Asp Tyr Tyr Ser Val Thr Lys Lys Leu Arg Leu His Tyr Tyr 100 105 110  Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120 125  (2) INFORMATION FOR SEQ ID NO: 55:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA to mRNA  (iii) HYPOTHETICAL: NO  (v) FRAGMENT TYPE: N-terminal  (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor	
Ala Arg Asp Tyr Tyr Ser Val Thr Lys Lys Leu Arg Leu His Tyr Tyr 100 105 110  Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120 125  (2) INFORMATION FOR SEQ ID NO: 55:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA to mRNA  (iii) HYPOTHETICAL: NO  (iv) ANTI-SENSE: NO  (v) FRAGMENT TYPE: N-terminal  (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor	
Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120 125  (2) INFORMATION FOR SEQ ID NO: 55:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA to mRNA  (iii) HYPOTHETICAL: NO  (iv) ANTI-SENSE: NO  (v) FRAGMENT TYPE: N-terminal  (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor	
(2) INFORMATION FOR SEQ ID NO: 55:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA to mRNA  (iii) HYPOTHETICAL: NO  (iv) ANTI-SENSE: NO  (v) FRAGMENT TYPE: N-terminal  (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor	
<ul> <li>(i) SEQUENCE CHARACTERISTICS: <ul> <li>(A) LENGTH: 315 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul> </li> <li>(ii) MOLECULE TYPE: cDNA to mRNA</li> <li>(iii) HYPOTHETICAL: NO</li> <li>(iv) ANTI-SENSE: NO</li> <li>(v) FRAGMENT TYPE: N-terminal</li> <li>(vi) ORIGINAL SOURCE: <ul> <li>(A) ORGANISM: Homo sapiens</li> <li>(C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor</li> </ul> </li> </ul>	
(A) LENGTH: 315 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA to mRNA  (iii) HYPOTHETICAL: NO  (iv) ANTI-SENSE: NO  (v) FRAGMENT TYPE: N-terminal  (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor	(2) INFORMATION FOR SEQ ID NO: 55:
<ul> <li>(iii) HYPOTHETICAL: NO</li> <li>(iv) ANTI-SENSE: NO</li> <li>(v) FRAGMENT TYPE: N-terminal</li> <li>(vi) ORIGINAL SOURCE: <ul> <li>(A) ORGANISM: Homo sapiens</li> <li>(C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor</li> </ul> </li> </ul>	<ul><li>(A) LENGTH: 315 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li></ul>
<ul> <li>(iv) ANTI-SENSE: NO</li> <li>(v) FRAGMENT TYPE: N-terminal</li> <li>(vi) ORIGINAL SOURCE: <ul> <li>(A) ORGANISM: Homo sapiens</li> <li>(C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor</li> </ul> </li> </ul>	(ii) MOLECULE TYPE: cDNA to mRNA
<ul> <li>(v) FRAGMENT TYPE: N-terminal</li> <li>(vi) ORIGINAL SOURCE: <ul> <li>(A) ORGANISM: Homo sapiens</li> <li>(C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor</li> </ul> </li> </ul>	(iii) HYPOTHETICAL: NO
<ul><li>(vi) ORIGINAL SOURCE:</li><li>(A) ORGANISM: Homo sapiens</li><li>(C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor</li></ul>	(iv) ANTI-SENSE: NO
<ul><li>(A) ORGANISM: Homo sapiens</li><li>(C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor</li></ul>	(v) FRAGMENT TYPE: N-terminal
	<ul><li>(A) ORGANISM: Homo sapiens</li><li>(C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor</li></ul>

(E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD1 (B) CLONE: LD1-6-17 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 2 (B) MAP POSITION: p11 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..315 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(64..96, 142..162, 259..285) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55: GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 10 15 5 GTC ACC ATC ACT TGC CGG GCA AGT CAG GGC ATT AGA AAT GAT TTA ACC Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Thr 20 25 30 TGG TAT CAG CAA AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC TAT GCT 144 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala 40 35 GCA TCC AAT TTA CAA AGT GGG GTC CCA TCA AGG TTC AGC GGC AGT GGA Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 60 50 55 TCT GGC ACA GAT TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT GAA GAT

240 Ser Gly Thr Asp Phe 65 70	Thr Leu Thr Ile So	er Ser Leu Gln Pro Glu Asp 80		,
		CAA GAT AAC AAT TTC C Asn Asn Phe Pro Tyr Thr Phe 95	CG TAC ACT TTT	288
GGC CAG GGG AC Gly Gln Gly Thr Lys 100		G ATC AAA	315	
(2) INFORMATION	FOR SEQ ID NO	): 56:		
. , _		TICS:		
(ii) MOLECULE (xi) SEQUENCE	•	SEQ ID NO: 56:		
Val Met Thr Gln Ser 1 5	Pro Ser Ser Leu S	Ser Ala Ser Val Gly Asp Arg 15		
Val Thr Ile Thr Cys 2	Arg Ala Ser Gln G 25 30	aly Ile Arg Asn Asp Leu Thr		
	Pro Gly Lys Ala I 40 45	Pro Lys Leu Leu Ile Tyr Ala		
Ala Ser Asn Leu Gln 50 55	Ser Gly Val Pro S 60	Ser Arg Phe Ser Gly Ser Gly		
Ser Gly Thr Asp Phe	Thr Leu Thr Ile S	Ser Ser Leu Gln Pro Glu Asp 80		
Phe Ala Thr Tyr Tyr 85	Cys Leu Gln Asp 90	Asn Asn Phe Pro Tyr Thr Phe 95		
Gly Gln Gly Thr Lys 100	Leu Glu Ile Lys 105			
(2) INFORMATION	FOR SEQ ID NO	D: 57:		

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 375 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
  - (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
  - (D) DEVELOPMENTAL STAGE: adult
  - (E) HAPLOTYPE: diploid
  - (G) CELL TYPE: Peripheral lymphocyte B
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA library, LD1 and LD2
  - (B) CLONE: LD1/2-6-3
- (viii) POSITION IN GENOME:
  - (A) CHROMOSOME/SEGMENT: chromosome 14
  - (B) MAP POSITION: q32.3
  - (C) UNITS: Chromosome band number
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION:1..375
  - (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"
- (ix) FEATURE:
  - (A) NAME/KEY: CDR1, CDR2, CDR3
  - (B) LOCATION:join(91..105, 148..198, 295..342)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG 48

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly

15 1 5 10 TCC CTG AGA GTC GCC TGT GTA GCG TCT GGA TTC ACC TTC AGG AAT TTT 96 Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe 20 25 GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 40 45 GCT TTT ATT TGG TTT GAT GCA AGT AAT AAA GGA TAT GGA GAC TCC GTT Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val 50 55 60 AAG GGC CGA TTC ACC GTC TCC AGA GAC AAT TCC AAG AAC ACG CTC TAT 240 Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 70 75 CTG CAA ATG AAC GGC CTG AGA GCC GAA GAC ACG GCT GTA TAT TAT TGT Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95 GCG AGA GAG AAG GCG GTT CGG GGA ATT AGT AGA TAC AAC TAC TAC ATG Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 110 100 105 375 GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120 125 (2) INFORMATION FOR SEQ ID NO: 58: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

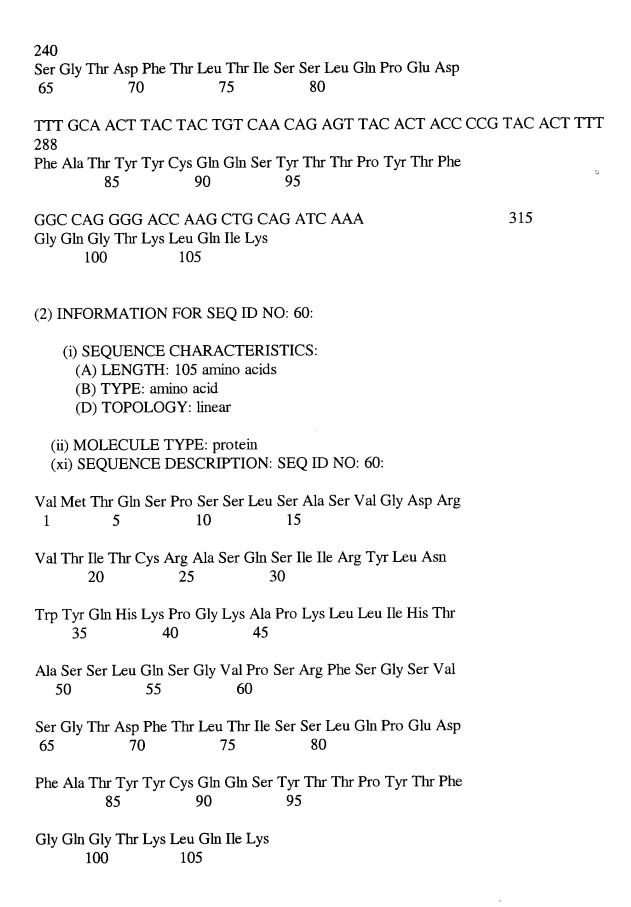
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 1 5 10 15
Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe 20 25 30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45
Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val 50 55 60
Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 65 70 75 80
Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95
Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 100 105 110
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120 125
(2) INFORMATION FOR SEQ ID NO: 59:
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 315 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>
(ii) MOLECULE TYPE: cDNA to mRNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(v) FRAGMENT TYPE: N-terminal
<ul> <li>(vi) ORIGINAL SOURCE:</li> <li>(A) ORGANISM: Homo sapiens</li> <li>(C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor</li> <li>(D) DEVELOPMENTAL STAGE: adult</li> <li>(E) HAPLOTYPE: diploid</li> </ul>

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(G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD1 and LD2 (B) CLONE: LD1/2-6-3 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 2 (B) MAP POSITION: p11 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..315 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(64..96, 142..162, 259..285) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59: GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 10 15 1 5 GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT ATC AGA TAT TTA AAT Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn 20 25 30 TGG TAT CAG CAC AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC CAT ACT 144 Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Thr 35 40 45 GCA TCC AGT TTG CAA AGT GGG GTC CCG TCA AGG TTC AGT GGC AGT GTA Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val 55 60 50 TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT GAA GAT



## (2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 375 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
  - (C) INDIVIDUAL ISOLATE: hyperimmune Rhesud D donor
  - (D) DEVELOPMENTAL STAGE: adult
  - (E) HAPLOTYPE: diploid
  - (G) CELL TYPE: Peripheral lymphocyte B
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA library, LD1 and LD2
  - (B) CLONE: LD1/2-2-33
- (viii) POSITION IN GENOME:
  - (A) CHROMOSOME/SEGMENT: chromosome 14
  - (B) MAP POSITION: q32.3
  - (C) UNITS: Chromosome band number
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION:1..375
  - (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"
- (ix) FEATURE:
  - (A) NAME/KEY: CDR1, CDR2, CDR3
  - (B) LOCATION:join(91..105, 148..198, 295..342)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG

48 Gln Val Lys Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 1 5 10 15	
TCC CTG AGA GTC GCC TGT GTA GCG TCT GGA TTC ACC TTC AGG AAT TTT Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe 20 25 30	96
GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG 144	
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45	
GCT TTT ATT TGG TTT GAT GCA AGT AAT AAA GGA TAT GGA GAC TCC GTT 192	
Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val 50 55 60	
AAG GGC CGA TTC ACC GTC TCC AGA GAC AAT TCC AAG AAC ACG CTC TAT 240	
Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 65 70 75 80	
CTG CAA ATG AAC GGC CTG AGA GCC GAA GAC ACG GCT GTA TAT TAT TGT 288	
Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  85 90 95	
GCG AGA GAG AAG GCG GTT CGG GGA ATT AGT AGA TAC AAC TAC TAC ATG 336	
Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met  100 105 110	
GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA  Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  115 120 125	
(2) INFORMATION FOR SEQ ID NO: 62:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 125 amino acids</li><li>(B) TYPE: amino acid</li><li>(D) TOPOLOGY: linear</li></ul>	

(ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62: Gln Val Lys Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 10 Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe 25 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 40 Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val 55 Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 70 75 Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 105 110 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 120 125 (2) INFORMATION FOR SEQ ID NO: 63: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens

(C) INDIVIDUAL ISOLATE: hyperimmune Resus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (C) CELL TYPE: Parishard lymphaguta P
(G) CELL TYPE: Peripheral lymphocyte B
(vii) IMMEDIATE SOURCE:  (A) LIBRARY: cDNA library, LD1 and LD2  (B) CLONE: LD1/2-6-33
<ul> <li>(viii) POSITION IN GENOME:</li> <li>(A) CHROMOSOME/SEGMENT: chromosome 2</li> <li>(B) MAP POSITION: p11</li> <li>(C) UNITS: Chromosome band number</li> </ul>
<ul><li>(ix) FEATURE:</li><li>(A) NAME/KEY: CDS</li><li>(B) LOCATION:1315</li><li>(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"</li></ul>
(ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(6496, 142162, 259285)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:
GTG ATG ACC CAG TCT CCA TCC TTC CTG TCT GCA TCT GTA GGA GAC AGA 48
Val Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp Arg 1 5 10 15
GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT ATC AGA TAT TTA AAT 96
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn 20 25 30
TGG TAT CAG CAC AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC CAT GCT 144
Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Ala 35 40 45
GCA TCC AGT TTG CAA AGT GGG GTC CCG TCA AGG TTC AGT GGC AGT GTA 192
Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val 50 55 60

TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT GAA GAT Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 80 75 65 70 TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC ACT ACC CCG TAC ACT TTT Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Tyr Thr Phe 90 95 85 GGC CAG GGG ACC AAG CTG CAG ATC AAA 315 Gly Gln Gly Thr Lys Leu Gln Ile Lys 100 105 (2) INFORMATION FOR SEQ ID NO: 64: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64: Val Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp Arg 1 5 10 15 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn 20 25 Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Ala 40 35 Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val 50 55 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 65 70 75 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Tyr Thr Phe 90 85 Gly Gln Gly Thr Lys Leu Gln Ile Lys 100 105